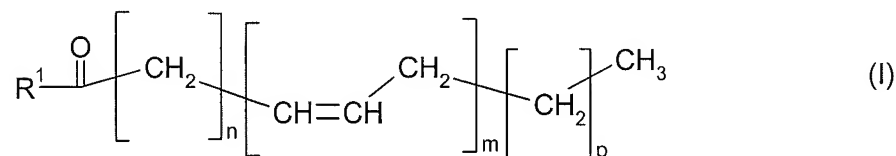


AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Currently amended) A process for the production of compounds of the general formula I

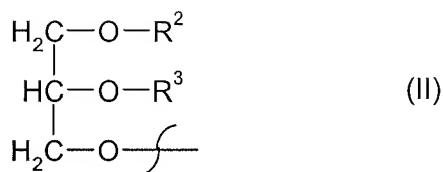


in the seed of transgenic plants with a content of at least 20% by weight based on the total lipid content, which comprises the following process steps:

- a) introducing, into the organism, at least one nucleic acid sequence which encodes a polypeptide with $\Delta 6$ -desaturase activity,
- b) introducing, into the organism, at least one nucleic acid sequence which encodes a polypeptide with $\Delta 6$ -elongase activity,
- c) introducing, into the organism, at least one nucleic acid sequence which encodes a polypeptide with $\Delta 5$ -desaturase activity,
- d) introducing, into the organism, at least one nucleic acid sequence which encodes a polypeptide with $\Delta 5$ -elongase activity that elongates only unsaturated C^{20} -fatty acids, and
- e) introducing, into the organism, at least one nucleic acid sequence which encodes a polypeptide with $\Delta 4$ -desaturase activity, and

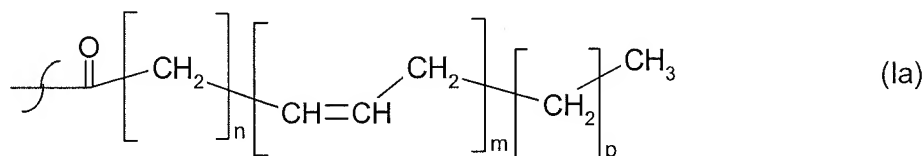
wherein the variables and substituents in formula I have the following meanings:

$\text{R}^1 =$ hydroxyl, coenzyme A (thioester), lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol, sphingo base or a radical of the general formula II



$\text{R}^2 =$ hydrogen, lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol or saturated or unsaturated $\text{C}_2\text{-C}_{24}$ -alkylcarbonyl,

$\text{R}^3 =$ hydrogen, saturated or unsaturated $\text{C}_2\text{-C}_{24}$ -alkylcarbonyl, or R^2 and R^3 independently of one another are a radical of the general formula Ia:



in which

$n = 2, 3, 4, 5, 6, 7$ or 9 , $m = 2, 3, 4, 5$ or 6 and $p = 0$ or 3 ,

and wherein the at least one nucleic acid sequence which encodes a polypeptide with $\Delta 5$ -elongase activity comprises:

- i) the nucleic acid sequence of SEQ ID NO: 67, 83, or 113;
 - ii) a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 68, 84, or 114;
 - iii) a nucleic acid sequence having at least 50% identity to the nucleic acid sequence of SEQ ID NO: 67, 83, or 113; or
 - iv) a nucleic acid sequence encoding an amino acid sequence having at least 50% identity to SEQ ID NO: 68, 84, or 114.
2. (Original) The process according to claim 1, wherein the variables n , m and p have the following meanings:
 $n = 2, 3$ or 5 , $m = 4, 5$ or 6 and $p = 0$ or 3 .
 3. (Previously presented) The process according to claim 1, wherein, in formula I, the

variables n, m and p have the following meanings:

- (a) $m = 4$, $n = 3$, $p = 3$ and the compound is arachidonic acid,
 - (b) $m = 5$, $n = 3$, $p = 0$ and the compound is eicosapentaenoic acid,
 - (c) $m = 5$, $n = 5$, $p = 0$ and the compound is docosapentaenoic acid, or
 - (d) $m = 6$, $n = 3$, $p = 0$ and the compound is docosahexaenoic acid.
4. (Previously presented) The process according to claim 2, wherein, in the seed of the transgenic plant, the content of all compounds of the formula I together amounts to at least 27% by weight based on the total lipid content.
5. (Previously presented) The process according to claim 3, wherein, in the seed of the transgenic plant, the docosahexaenoic acid content amounts to at least 1% by weight based on the total lipid content.
6. (Currently amended) The process according to claim 1, wherein the nucleic acid sequences which encode polypeptides with $\Delta 6$ -desaturase, $\Delta 6$ -elongase, $\Delta 5$ -desaturase, ~~$\Delta 5$ -elongase~~ or $\Delta 4$ -desaturase activity are selected from the group consisting of:
- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 11, SEQ ID NO: 27, SEQ ID NO: 41, ~~SEQ ID NO: 53, SEQ ID NO: 83, SEQ ID NO: 113,~~ or SEQ ID NO: 193,
 - b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence[[s]] shown in SEQ ID NO: 12, SEQ ID NO: 28, SEQ ID NO: 42, ~~SEQ ID NO: 54, SEQ ID NO: 84, SEQ ID NO: 114,~~ or SEQ ID NO: 194, and
 - c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 11, SEQ ID NO: 27, SEQ ID NO: 41, ~~SEQ ID NO: 53, SEQ ID NO: 83, SEQ ID NO: 113,~~ or SEQ ID NO: 193, which encode polypeptides with at least 40% 50% identity at the amino acid level with SEQ ID NO: 12, SEQ ID NO: 28, SEQ ID NO: 42, ~~SEQ ID NO: 54, SEQ ID NO: 84, SEQ ID NO: 114,~~ or SEQ ID NO: 194, and which have $\Delta 6$ -desaturase, $\Delta 6$ -elongase, $\Delta 5$ -desaturase, ~~$\Delta 5$ -elongase~~ or $\Delta 4$ -desaturase activity.

7. (Withdrawn) The process according to claim 1, wherein a nucleic acid sequence which encodes polypeptides with ω 3-desaturase activity, selected from the group consisting of:
- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, or
 - b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 88 or SEQ ID NO: 106, or
 - c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, which encode polypeptides with at least 60% identity at the amino acid level with SEQ ID NO: 88 or SEQ ID NO: 106 and which have ω 3-desaturase activity
- is additionally introduced into the transgenic plant.
8. (Withdrawn) The process according to claim 1, wherein a nucleic acid sequence which encodes polypeptides with Δ 12-desaturase activity, selected from the group consisting of:
- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 107, SEQ ID NO: 109 or SEQ ID NO: 195, or
 - b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 108, SEQ ID NO: 110 or SEQ ID NO: 196, or
 - c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 107, SEQ ID NO: 109 or SEQ ID NO: 195, which encode polypeptides with at least 60% identity at the amino acid level with SEQ ID NO: 108, SEQ ID NO: 110 or SEQ ID NO: 196 and which have Δ 12-desaturase activity
- is additionally introduced into the transgenic plant.
9. (Withdrawn) The process according to claim 1, wherein a nucleic acid sequence which encodes proteins of the biosynthetic pathway of the fatty acid or lipid metabolism selected from the group acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid

- hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s) is additionally introduced into the transgenic plant.
10. (Previously presented) The process according to claim 1, wherein the substituents R^2 or R^3 independently of one another are saturated or unsaturated C_{18} - C_{22} -alkylcarbonyl.
 11. (Previously presented) The process according to claim 1, wherein the substituents R^2 or R^3 independently of one another are unsaturated C_{18} -, C_{20} - or C_{22} -alkylcarbonyl with at least two double bonds.
 12. (Previously presented) The process according to claim 1, wherein the transgenic plant is selected from the group consisting of an oil-producing plant, a vegetable plant and an ornamental.
 13. (Previously presented) The process according to claim 1, wherein the transgenic plant is selected from the group of the plant families consisting of: Anacardiaceae, Asteraceae, Boraginaceae, Brassicaceae, Cannabaceae, Compositae, Cruciferae, Cucurbitaceae, Elaeagnaceae, Euphorbiaceae, Fabaceae, Geraniaceae, Gramineae, Leguminosae, Linaceae, Malvaceae, Moringaceae, Marchantiaceae, Onagraceae, Olacaceae, Oleaceae, Papaveraceae, Piperaceae, Pedaliaceae, Poaceae and Solanaceae.
 14. (Previously presented) The process according to claim 1, wherein the compounds of the general formula I are isolated from the transgenic plant in the form of their oils, lipids or free fatty acids.
 - 15-63. (Cancelled)
 64. (Previously presented) The process according to claim 1, wherein the polypeptide with $\Delta 5$ -elongase activity elongates only unsaturated C_{20} -fatty acids with one double bond in the $\Delta 5$ -position.
 65. (Previously presented) The process according to claim 1, wherein the compounds of the general formula I comprise fatty acids having 20 or 22 carbon atoms in the fatty acid chain.
 66. (Previously presented) The process according to claim 1, wherein the organism is

selected from the group consisting of soybean, peanut, oilseed rape, canola, linseed, evening primrose, mullein, thistle, hazelnut, almond, macadamia, avocado, bay, wild roses, pumpkin/squash, pistachios, sesame, sunflower, safflower, borage, maize, poppy, mustard, hemp, castor-oil plant, olive, Calendula, Punica, oil palm, walnut and coconut.

67. (New) The process according to claim 1, wherein the at least one nucleic acid sequence which encodes a polypeptide with $\Delta 5$ -elongase activity comprises a nucleic acid sequence encoding an amino acid sequence having at least 80% identity to SEQ ID NO: 68, 84, or 114.
68. (New) The process according to claim 1, wherein the at least one nucleic acid sequence which encodes a polypeptide with $\Delta 5$ -elongase activity comprises a nucleic acid sequence encoding an amino acid sequence having at least 90% identity to SEQ ID NO: 68, 84, or 114.
69. (New) The process according to claim 1, wherein the at least one nucleic acid sequence which encodes a polypeptide with $\Delta 5$ -elongase activity comprises a nucleic acid sequence encoding an amino acid sequence having at least 95% identity to SEQ ID NO: 68, 84, or 114.